Animal Genetics, 2000, **31**, 206–209

SHORT COMMUNICATION

Consensus and comprehensive linkage maps of bovine chromosome 7

Z Gu, L Gomez-Raya, D I Våge, K Elo, W Barendse, G Davis, M Grosz, G Erhardt, E Kalm, N Reinsch, S M. Kappes, R T Stone, S K Davis, J F Taylor, B W Kirkpatrick

Z Gu
B W Kirkpatrick
Department of Animal Sciences, University of Wisconsin-Madison, WI 53706 USA
L Gomez-Raya
D I Våge
Department of Animal Science, Agricultural University of Norway, N-1432 Aas, Norway
K Elo
Agricultural Research Centre MTT, Animal Production Research, Animal Breeding, FIN-31600 Jokioinen, Finland
W Barendse
CSIRO Molecular Animal Genetics Centre, Brisbane, Australia
G Davis
CSIRO Tropical Agriculture, Molecular Animal Genetics Centre, Brisbane, QLD 4072, Australia
M Grosz
USDA ARS Fort Keogh LARRL, Miles City, MT, USA
G Erhardt
E Kalm
Department of Animal Breeding and Genetics, Justus-Liebig-University Giessen, Ludwigstr. 21, D-35390 Giessen, Germany
N Reinsch
Institut für Tierzucht und Tierhaltung der Christian-Albrechts-Universität, D-24098 Kiel, Germany
S M Kappes
R T Stone
USDA Meat Animal Research Center, Clay Center, NE, USA
S K Davis
J F Taylor
Texas A & M University, College Station TX 77843-2471, USA

Summary

The objective of this project was to integrate the currently available linkage maps for bovine chromosome 7 (BTA7) by combining data sets from eight research groups. A total of 54 unique markers were typed in eight pedigrees. Multilocus linkage analysis with CRI-MAP produced a bovine chromosome 7 consensus framework map of 27 loci ordered with odds greater than 1000 : 1. Furthermore, we present a bovine chromosome 7 comprehensive map integrating 54 loci. The locus order is in general agreement with the recently published linkage maps except for one discrepancy. The order of loci *BM9289*, *BMS713*, and *ILSTS001* was reversed in the consensus framework map relative to the published USDA-MARC bovine chromosome 7 linkage map.

Keywords: cattle, framework map, genetic marker, genetics

Several bovine linkage maps have been constructed using independent pedigrees and a partially overlapping set of markers. Integration of these maps is of great importance. An integrated map serves as a bridge of communication among mapping research groups by working out discrepancies in locus order between the various maps and building statistical support for the location of markers that are less supported in just one data set.

In 1995, Eggen and Fries integrated the bovine cytogenetic map with the two most comprehensive linkage maps at that time (Barendse *et al.* 1994; Bishop *et al.* 1994). Unfortunately, the number of commonly mapped loci between the two linkage maps was so limited that most of the genome regions were not integrated. For bovine chromosome 7, *RASA* was the only coding gene mapped by Bishop *et al.* (1994) that was also physically mapped. There were three markers on the Barendse *et al.* (1994) chromosome 7 map, and two of them were also mapped by Bishop *et al.* (1994). Most regions of the bovine chromosome 7 linkage and physical maps were left unconnected (Eggen & Fries 1995). Subsequent efforts to create a more decent linkage map (Barendse *et al.* 1997) and to physically map additional loci (Ferretti *et al.* 1997) have extended the tie between physical and linkage maps for bovine chromosome 7.

The subsequent availability of more dense linkage maps (Barendse *et al.* 1997; Kappes *et al.* 1997) increases the need for building the consensus linkage map for each bovine chromosome. Most typed markers were not in common between the most comprehensive bovine linkage maps and there is some disagreement in locus order between maps. Thus a consensus map serves as a way of integrating linkage maps and helps to solve locus order discrepancies. In this study, we present the results of analysis of data submitted by eight research groups. The goal was to construct a consensus framework map of bovine chromosome 7 and a comprehensive map including all polymorphic loci.

Eight genotype data sets were submitted by research groups from around the world as part of an International Society for Animal Genetics-sponsored effort to develop consensus bovine linkage maps. Data were provided for the International Bovine Reference Pedigrees (IBRP), USDA Meat Animal Research Centre Bovine Pedigrees (USDA-MARC), Texas A & M University Angleton Families (TAMU), Agricultural Research Centre MTT pedigrees (MTT), CSIRO Tropical Agriculture pedigrees (CSIRO-TROP), USDA ARS Fort Keogh LARRL pedigrees (USDA-LARRL), German Cattle Breeding Organisation pedigrees (ADR), and Norwegian Cattle Pedigrees (NCM). The data were provided in CRI-MAP format. Among the data sets, the number of offspring varied from 152 to 1716 and the number of markers typed ranged from 6 to 43.

For each data set, a framework map consisting only of loci whose location could be mapped

Correspondence: B W Kirkpatrick.

Accepted 12 January 2000

with interval support of LOD 3 was built. Data from TAMU, MARC, and IBRP contained information from both male and female meioses, and a sex-averaged framework map was built for each of those data sets. ADR, MTT, NCM, CSIRO-TROP and LARRL contained segregation information from male parents only and male-specific maps were constructed for those data sets.

A consensus map was defined to include loci whose map location had interval support of LOD ≥ 3 and which appear in at least two data sets. As a first step in building a consensus map the eight data sets were merged into one large data set, yielding an integrated data set contained a total of 60 families and 54 unique markers. Two-point linkage analysis was then performed for each pair of loci using CRI-MAP. Markers with no recombination events between them were identified and subsequently treated as one locus. Thirty-two potential consensus loci were grouped into three overlapping linkage groups based on the two-point analysis results. The strategy of dividing the loci into linkage groups facilitated the subsequent ordering of the markers by limiting the number of loci under evaluation. Third, for each linkage group, the 'build' command of CRI-MAP was used to construct a map starting from a pair of linked loci by sequentially incorporating additional loci using a statistical threshold of LOD ≥ 30 for discarding locus orders during the 'build' process. Fourth, the order of loci obtained from the 'build' procedure was used as a starting point to examine local rearrangements of two or three adjacent loci. If a LOD score difference between a permuted order and the reference order was less than 3, then one of the loci involved in the rearrangement was dropped until all permuted orders were at least 1000 times less likely than the reference order. Finally, the three framework maps were integrated by merging the overlapping linkage groups. The map was again tested for rearrangement of two or three adjacent loci.

The purpose of a comprehensive map is to estimate the order of all syntenic loci. Thus no minimum interval support is required in the construction of the comprehensive map assuming all loci are syntenic (Ott 1991). Based on the definition of a comprehensive map, the CRI-MAP command 'all' was used to incorporate all remaining loci relative to the loci in the framework map. In this case, the consensus map served as the starting point for construction of the comprehensive map.

There were 54 unique loci in the combined data set. Thirty-two of them appeared in at least two data sets and were used to construct the consensus map. Of the 32 loci, 27 could be ordered with interval support of LOD 3. Thus a chromosome 7 consensus map was built with 27 framework loci (Table 1). There were no discrepancies in locus order between the consensus framework map and the individual framework maps from each data set. However,

Table 1. Consensus framework map with the genetic distance and interval support

Markers	Cumulative Kosambi distance (cM)	Interval support (LOD)
BM7160	0.0	
		46.35
RM012	9.6	
		23.30
ILSTS001	13.4	
		3.48
BMS713	14.9	
		6.18
BM9289	15.9	
		8.39
IDVGA-90	17.4	
		44.16
RM006	24.6	
		6.16
BM2607	29.7	
		3.22
IL4	31.6	
		15.40
BM6105	34.6	
		9.61
TGLA303	37.0	
		27.14
BM741	48.0	
		41.17
UWCA20	56.4	
		4.35
CSSM29	58.1	
		8.48
BM6117	61.4	
		56.25
BMS2258	74.4	
		16.67
INRA192	80.8	
		11.47
BMS1331	88.0	
		9.79
OARAE129	95.2	
		11.78
RASA/BM9065/BM7208	101.5	
		61.24
ILSTS006	114.2	
		9.03
CAST/BM1520	119.9	
		5.00
INRA053	124.6	
		25.84
BL1043	137.0	

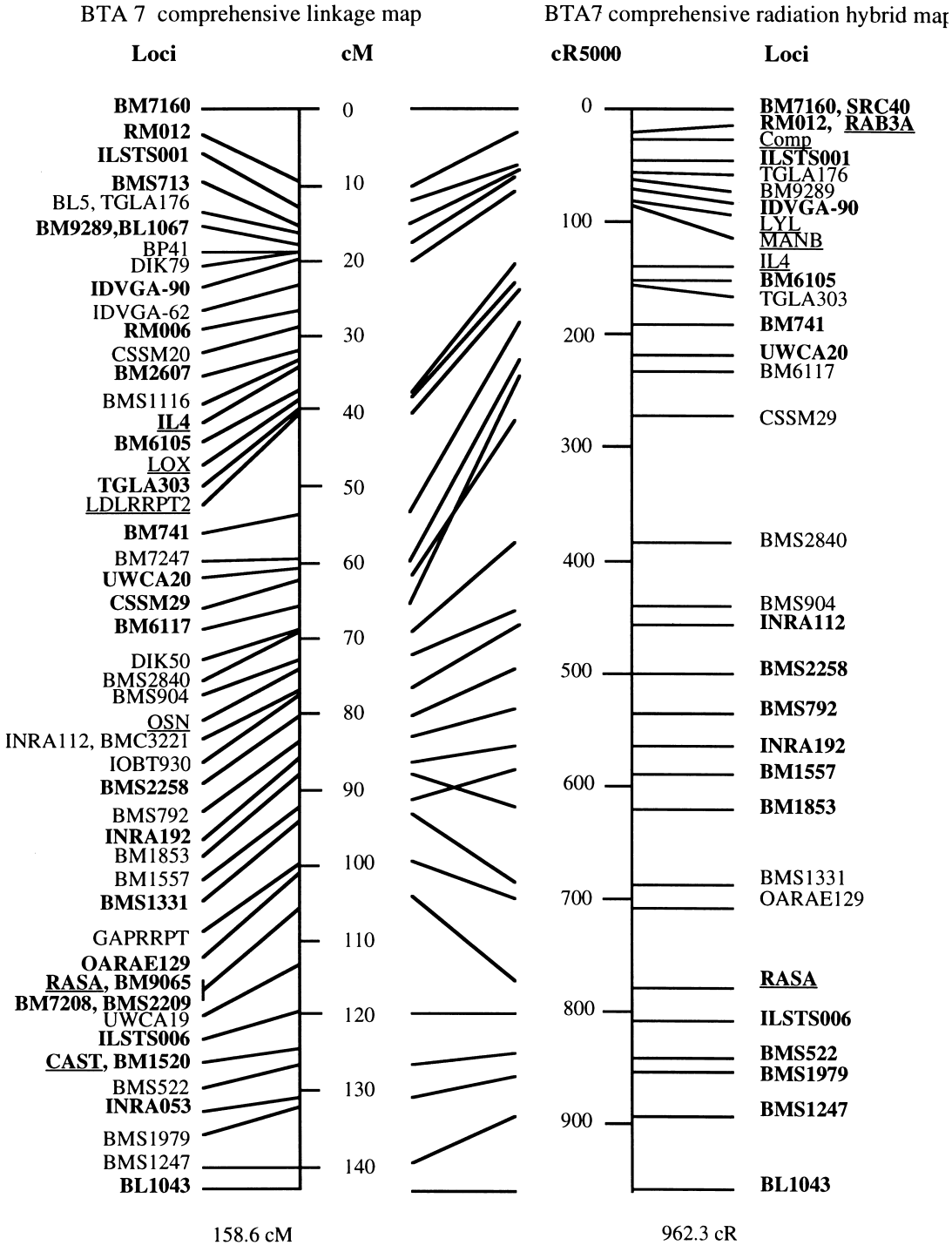

Fig. 1. Comparison of the comprehensive linkage map and radiation hybrid map (Gu *et al.* 1999) of bovine chromosome 7. Locus symbols in boldface are framework loci whose order is supported by odds of 1000 : 1. Underlined symbols are Type I loci (genes).

compared to the published bovine linkage maps, a difference in locus order was discovered between the consensus map and the USDA map (Kappes *et al.* 1997). In the USDA-MARC map, the locus order of *RM012–BM9289–BMS713–ILSTS001–RM006* was reported. In the consensus map, the order of loci *ILSTS001*, *BMS713*, and *BM9289* was inverted relative to the USDA map. The locus order found here for the consensus map is in agreement with that reported for the bovine chromosome 7 radiation hybrid map (Gu *et al.* 1999; Fig. 1). Locus *IDVGA-90* was included in the submitted USDA data set, but it did not appear in the published USDA-MARC map. Inclusion of this locus was helpful in determining a locus order consistent with that observed in the radiation hybrid map.

Based on the consensus map, the best location of the remaining 27 loci were identified in the construction of the comprehensive map (Fig. 1). Although there is limited statistical support for the locus order in this map, the comprehensive map provides useful information on marker location for future studies. Two discrepancies were observed between locus orders for the comprehensive linkage and radiation hybrid maps. The order of *BM6117* and *CSSM29* was inverted between the two maps, as was the order of *BM1557* and *BM1853*. Statistical support for the order observed for *BM6117* and *CSSM29* in the linkage map is greater than that for the radiation hybrid map, whereas the opposite is true for the order of *BM1557* and *BM1853*.

In summary, the consensus framework map incorporated 27 loci on bovine chromosome 7. There was a high level of support for the locus order on the consensus map. The comprehensive map reveals the best location for the remaining 27 loci based on the consensus map locus order. These results will be useful guides for future QTL mapping studies on bovine chromosome 7.

References

Barendse, W., Armitage, S.M., Kossarek, L.M., *et al.* (1994) A genetic linkage map of the bovine genome. *Nature Genetics* **6,** 22735.

Barendse, W., Vaiman, D., Kemp, S.J. *et al.* (1997) A medium-density genetic linkage map of the bovine genome. *Mammalian Genome* **8,** 218.

Bishop, M.D., Kappes, S.M., Keele, J.W. *et al.* (1994) A genetic linkage map for cattle. *Genetics* **136,** 61939.

Eggen, A. & Fries, R. (1995) An integrated cytogenetic and meiotic map of the bovine genome. *Animal Genetics* **26,** 21536.

Ferretti, L., Urquhart, B.G.D., Eggen, A. *et al.* (1997) Cosmid-derived markers anchoring the bovine genetic map to the physical map. *Mammalian Genome* **8,** 2936.

Gu, Z., Kirkpatrick, B.W. & Womack, J. (1999) A radiation hybrid map of bovine chromosome 7 and comparative mapping with human chromosome 19, p. arm. *Mammalian Genome* **10,** 11124.

Kappes, S.M., Keele, J.W., Stone, R.T. *et al.* (1997) A second-generation linkage map of the bovine genome. *Genome Research* **7,** 23549.

Ott, J. (1991) *Analysis of Human Genetic Linkage*. The John Hopkins University Press, Baltimore, MD.